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An Incremental Model for the Coreference Resolution Task of BioNLP 2011

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Abstract

We introduce our incremental coreference resolution system for the BioNLP 2011 Shared Task on Protein/Gene interaction. The benefits of an incremental architecture over a mention-pair model are: a reduction of the number of candidate pairs, a means to overcome the problem of underspecified items in pair-wise classification and the natural integration of global constraints such as transitivity. A filtering system takes into account specific features of different anaphora types. We do not apply Machine Learning, instead the system classifies with an empirically derived salience measure based on the dependency labels of the true mentions. The OntoGene pipeline is used for preprocessing.

1 Introduction

The Coreference Resolution task of BioNLP focused on finding anaphoric references to proteins and genes. Only antecedent-anaphora pairs are considered in evaluation and not full coreference sets. Although it might not seem to be necessary to generate full coreference sets, anaphora resolution still benefits from their establishment. Our incremental approach (Klenner et al., 2010) naturally enforces transitivity constraints and thereby reduces the number of potential antecedent candidates. The system achieved good results in the BioNLP 2011 shared task (Fig. 1)

Team	R	P	F1
A	22.18	73.26	34.05
Our model	21.48	55.45	30.96
B	19.37	63.22	29.65
C	14.44	67.21	23.77
D	3.17	3.47	3.31
E	0.70	0.25	0.37

Figure 1: Protein/Gene Coreference Task

2 Preprocessing: The OntoGene Pipeline

OntoGene’s text mining system is based on an internally-developed fast, broad-coverage, deep-

syntactic parsing system (Schneider, 2008). The parser is wrapped into a pipeline which uses a number of other NLP tools. The parser is a key component in a pipeline of NLP tools (Rinaldi et al., 2010), used to process input documents. First, in a pre-processing stage, the input text is transformed into a custom XML format, and sentences and tokens boundaries are identified. The OntoGene pipeline also includes a step of term annotation and disambiguation, which are not used for the BioNLP shared task, since relevant terms are already provided in both the training and test corpora. The pipeline also includes part-of-speech taggers, a lemmatizer and a syntactic chunker.

When the pipeline finishes, each input sentence has been annotated with additional information, which can be briefly summarized as follows: sentences are tokenized and their borders are detected; each sentence and each token has been assigned an ID; each token is lemmatized; tokens which belong to terms are grouped; each term is assigned a normal-form and a semantic type; tokens and terms are then grouped into chunks; each chunk has a type (NP or VP) and a head token; each sentence is described as a syntactic dependency structure. All this information is represented as a set of predicates and stored into the Knowledge Base of the system, which can then be used by different applications, such as the OntoGene Relation Miner (Rinaldi et al., 2006) and the OntoGene Protein-Protein Interaction discovery tool (Rinaldi et al., 2008).

3 Our Incremental Model for Coreference Resolution

```
1   for   i=1       to length(I)
2       for   j=1 to length(C)
3            $r_j$  := virtual prototype of coreference set  $C_j$ 
4           Cand := Cand  $\oplus$   $r_j$  if compatible( $r_j, m_i$ )
5       for   k= length(B) to 1
6            $b_k$  := the k-th licensed buffer element
7           Cand := Cand  $\oplus$   $b_k$  if compatible( $b_k, m_i$ )
8   if   Cand = {} then B := B  $\oplus$   $m_i$ 
9   if   Cand  $\neq$  {} then
10       $ante_i$  := most salient element of Cand
11      C      := augment(C,  $ante_i, m_i$ )
```

Figure 2: Incremental model: base algorithm

Fig. 2 shows the base algorithm. Let I be the chronologically ordered list of NPs, C be the set of coreference sets and B a buffer, where NPs are stored, if they are not anaphoric (but might be valid antecedents). Furthermore m_i is the current NP and \oplus means concatenation of a list and a single item. The algorithm proceeds as follows: a set of antecedent candidates is determined for each NP m_i (steps 1 to 7) from the coreference sets (r_j) and the buffer (b_k). A valid candidate r_j or b_k must be compatible with m_i . The definition of compatibility depends on the POS tags of the anaphor-antecedent pair. The most salient available candidate is selected as antecedent for m_i .

3.1 Restricted Accessibility of Antecedent Candidates

In order to reduce underspecification, m_i is compared to a virtual prototype of each coreference set (similar to e.g. (Luo et al., 2004; Yang et al., 2004; Rahman and Ng, 2009)). The virtual prototype bears morphologic and semantic information accumulated from all elements of the coreference set. Access to coreference sets is restricted to the virtual prototype. This reduces the number of considered pairs (from the cardinality of a set to 1).

3.2 Filtering based on Anaphora Type

Potentially co-referring NPs are extracted from the OntoGene pipeline based on POS tags. We then apply filtering based on anaphora type: Reflexive pronouns must be bound to a NP that is governed by the same verb. Relative pronouns are bound to the closest NP in the left context. Personal and possessive pronouns are licensed to bind to morphologically compatible antecedent candidates within a window of two sentences. Demonstrative NPs containing the lemmata 'protein' or 'gene' are licensed to bind to name containing mentions. Demonstrative NPs not containing the trigger lemmata can be resolved to string matching NPs preceding them¹.

3.3 Binding Theory as a Filter

We know through binding theory that 'modulator' and 'it' cannot be coreferent in the sentence "*Overexpression of protein inhibited stimulus-mediated transcription, whereas modulator enhanced it*". Thus, the pair 'modulator'-'it' need not be considered at all. We have not yet implemented a full-

blown binding theory. Instead, we check if the antecedent and the anaphor are governed by the same verb.

4 An Empirically-based Saliency Measure

Our saliency measure is a partial adaption of the measure from (Lappin and Leass, 1994). The saliency of a NP is solely defined by the saliency of the dependency label it bears. The saliency of a dependency label, D , is estimated by the number of true mentions (i.e. co-referring NPs) that bear D (i.e. are connected to their heads with D), divided by the total number of true mentions (bearing any D). The saliency of the label *subject* is thus calculated by:

$$\frac{\text{Number of true mentions bearing subject}}{\text{Total number of true mentions}}$$

We get a hierarchical ordering of the dependency labels (subject > object > pobject > ...) according to which antecedents are ranked and selected.

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¹As we do not perform anaphoricity determination of nominal NPs, we do not consider bridging anaphora (anaphoric nouns that are connected to their antecedents through semantic relations and cannot be identified by string matching).